IN THE SPECIFICATION:

Please amend paragraphs **[0011]**, **[0012]**, **[0021]**, **[0044]**, and **[0047]** as follows:

[0011] By a "*Plasmodium* AMA-1 ectodomain" is meant herein a part of a *Plasmodium* AMA-1 protein which is normally present between the N-terminal signal sequence and the transmembrane region of a naturally occurring *Plasmodium* AMA-1 protein. In *P. falciparum*, the ectodomain normally spans amino acid residues 25 to 545 of SEQ ID NO:7. In a preferred embodiment, an ectodomain of the invention spans an amino acid sequence corresponding to amino acid residues 25 to 545 of SEQ ID NO:7 in *P. falciparum*.

[0012] A functional part of a *Plasmodium* AMA-1 ectodomain is defined herein as a part which comprises at least one immunogenic property of the AMA-1 ectodomain in kind, not necessarily in amount. Preferably, the functional part comprises at least part of the prosequence, domain I, domain II and/or domain III of a *P. falciparum* AMA-1 ectodomain. More preferably, the functional part spans an amino acid sequence corresponding to amino acid residues 25-442, 97-318, 97-442, 97-545, 303-442, 303-544, and/or 419-544 of SEQ ID NO:7 in *P. falciparum*.

[0021] Figure 1 shows a nucleic acid of the invention, comprising the above-mentioned preferred characteristics. Thus, in one aspect, the present invention discloses an isolated and/or recombinant nucleic acid sequence encoding the *Plasmodium* AMA-1 ectodomain (SEQ ID NO:7) or a functional part, derivative, and/or analogue thereof, the nucleic acid comprising a sequence as depicted in Figure 1 (SEQ ID NO:6).

[0044] Figure 1 is a sequence of an isolated and/or recombinant nucleic acid (SEQ ID NO:6) of the present invention, encoding *Plasmodium* AMA-1 ectodomain ~~(SEQ ID NO:6)~~ (SEQ ID NO:7). Surprisingly, this sequence is very well expressed in *Pichia pastoris*, whereas a nucleic acid sequence encoding wild-type Pf AMA-1 ectodomain is not.

[0047] The sequence of gene Pf AMA-1 from the FVO strain that we have established, encodes a protein of 622 amino acid residues that has six potential N-glycosylation sites. Our previous experience with expressing Pf AMA-1 in baculovirus/insect cells as well as with expressing Pv AMA-1 in *P. pastoris* has shown that these N-glycosylation sites will be glycosylated in eukaryotic heterologous expression systems. As explained above, this is

undesirable since native Pf AMA-1 is not glycosylated. Therefore, we developed a variant that exploited the lack of conservation of N-glycosylation sites in published *Plasmodium* AMA-1 allele sequences. Asn 162 was changed to Lys that is present in that position in the Thai-Tn strain Pf AMA-1 (accession number M58547). Thr 288 was changed to Val (present in *P. vivax* and *P. knowlesi* AMA-1; accession numbers Y16950 and M61097); Ser 373 was changed to Asp (present in *P. knowlesi* AMA-1); Asn 422 and Ser 423 were changed to Asp and Lys, respectively (present in *P. knowlesi*, *P. vivax*, *P. chabaudi* (accession number M25248) and *P. fragile* AMA-1 (accession number M29898)) and Asn 499 was changed to [[Glu]] Gln (present in *P. chabaudi* AMA-1).